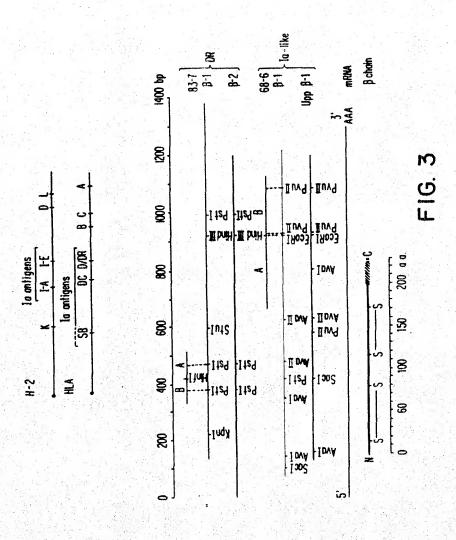
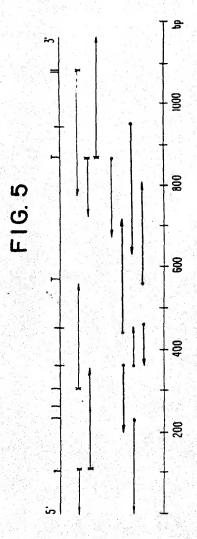


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Raji Cells extraction Poly A+ RNA size fractionation HLA-DR B-chain Poly A+RNA other RNAs FIG. 2 (1) reverse transcriptase (2) double stranding HLA-DR B-chain CDNA (ds) other CDNA (ds)'s (1) dc -tailing (2) Ligation (2) dG-tailing HLA-DR B- Chain C DNA insert + other hybrids THR made u) Transfection E. coli: HB101 competant (1) screening (3) Excision

HLA-DR B-Chain





47	68	131	173	215	257
L CTG	T 3 ACA	TACC	FTTC	F	999
C TGT	V GTG	DCAC	H	30 H CAC	V GTG
v GTG	ACA	6 6 6	c TGT	R AGA	DGAC
MATG	TTG	GCT	EGAG	EGAG	S AGC
	<b>₹</b> 800	F	S	L CTG	DGAC
CTCC	A GCA	A GCT	K	F	TTC
TCT	L	L	L	<b>8</b> 550	R TT CGC TT G. 5A
GTCC	S	R	10 L CTG	v GTG	F I
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CTGG	ပ္ ပ္	S AGC	L TTG	EGAG	EGAG
သသဗ္ဗ	GGA	L CTG	F	T ACG	EGAG
TCTG	P	v GTG	R CGT	20 G	CAG CAG
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(e)	K AAG	CTG.	R	F	r C T
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DR4,6 RHNYGVVESFTVQRRVHPQVTVYPAKTQPLQHHNLLV
DR2,2 -----Q-K----S-----DC ----QLELRT-L----E-T--1S-SR-EA-N-----

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## FIG 7

6TT CTC CCT GAG TGA GAC TCA CCT GCT CCT CTG GCC CCT GGT CCT GTC CTG TTC TCC AGC ATG GTG FGT CTG AAG FTC CCT GGA Gec Sec Fee Ate Bea Bet Ets Aca Sts Aca Ets Ats Sts Ets Ase Ice Cea Ets Bet Its Get Bes Bac Ace Esa Eca Est Ftc Its E 0 V K HI E G CT HI FIC TIC AAC GGG ACG GAG CGG GTG CGG TIC CTG GAC AGA TAC TIC TAT CAC CAA GAG EAG TAC LIC LE EN ANG REGION OF AND AND TO TO TO THE REST OF THE SECTION OF THE SECTION OF THE REST OF THE RES GG SG ATT EAR GTC AGG FGG TTC CGG AAC GGC CAG GAA GAG AAC GGG GTG GGG GTG TCC ACA GGC CTG ATC CAG AAT GGA GAC FGG

## FIG. 7A

ACC FIC CAG ACC CIG 616 ATG CIG SAA ACA GIT CCI CGG AGT GGA GAG GIT TAC ACC FGC CAA GIG EAG CAC CCA AGC CIG ACG AGC CCT CTC ACA GTG GAA TGG AGA GCA CGG TCT GAA TCT GCA CAG AGC AAG ATG CTG AGT GGA GTC GGG GGC TTC GTG CTG GGC CTG CTG

FIC CTT 666 GCC 666 CTG FTC ATC TAG FTG AGG AAT CAG AAA 66A CAC TCT 66A CTT CAG CCA ACA 66A FTC CTG AGG TGA AGT GAA

TIT CIC CGG ACC TGG TTG CTA CTG GTT CAG CAG CTC TGC AGA AAA TGT CCT CCC TTG TGG CTG CCT CAG CTC GTA CCT TTG

GAT GAC CAC ATT CAA GGA AGA ACC TTC TGC CCC AGC TTT GCA GGA TGA AAC ACT TCC CCG CTT GGC TCT CAT TCT TCC ACA AGA GAG

16A AGT CCC AGC ATT AAT 66C AGC CCC TCA TCT TCC AAG TTT TGT GCT CCC CTT TAC CTA ATG CTT CCT GCG TCC CAT GCA TCT GTA

FIG. 8

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## FIG. 9

Region I

AA 8 9 10 11 12 13 14

L E L L K S E

HLA-DR-\$\beta\_{-A}\$ TTG GAG CTG CTT AAG TCT GAG

HLA-DR-\$\beta\_{-}\$ TTG GAG CAG GTT AAA CAT GAG

L E Q V K H E

Region II

AA 26 27 28 29 30 31 32

F L E R H F H

HLA-DR-\$\beta\_{-A}\$ TTC CTG GAG AGA CAC TTC CAT

TTC CTG GAG AGA TAC TTC TAT

F L D R Y F Y

Region III

AA 72 73 74 75 76 77 78

R G Q V D N Y

HLA-DR-\$\beta\_{-A}\$ CGG GGC CAG GTG GAC AAT TAC

GGG GGC GGG GTG GAC ACC TAC

R A A V D T V